



SEQUENCE LISTING

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YANG, ANNIE
LODA, MASSIMO
SIGNORETTI, SABINA
CRUM, CHRISTOPHER

<120> CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
RELATED THERETO

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<140> 09/538,106
<141> 2000-03-29

<150> 09/174,493
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<150> 60/087,216
<151> 1998-05-29

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<170> PatentIn Ver. 2.1

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Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His			
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Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln His Gln His Leu			
340	345	350	
ctt cag aaa cag acc tca ata cag tct cca tct tca tat ggt aac agc		1104	
Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser			
355	360	365	
tcc cca cct ctg aac aaa atg aac agc atg aac aag ctg cct tct gtg		1152	
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val			
370	375	380	
agc cag ctt atc aac cct cag cag cgcc aac gcc ctc act cct aca acc		1200	
Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr			
385	390	395	400
att cct gat ggc atg gga gcc aac att ccc atg atg ggc acc cac atg		1248	
Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met			
405	410	415	
cca atg gct gga gac atg aat gga ctc agc ccc acc cag gca ctc cct		1296	
Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro			
420	425	430	
ccc cca ctc tcc atg cca tcc acc tcc cac tgc aca ccc cca cct ccg		1344	
Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro			
435	440	445	
tat ccc aca gat tgc agc att gtc agt ttc tta gcg agg ttg ggc tgt		1392	
Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys			
450	455	460	
tca tca tgt ctg gac tat ttc acg acc cag ggg ctg acc acc atc tat		1440	
Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr			
465	470	475	480
cag att gag cat tac tcc atg gat gat ctg gca agt ctg aaa atc cct		1488	
Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro			
485	490	495	
gag caa ttt cga cat gcg atc tgg aag ggc atc ctg gac cac cgg cag		1536	
Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln			
500	505	510	
ctc cac gaa ttc tcc tcc cct tct cat ctc ctg cgg acc cca agc agt		1584	
Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser			
515	520	525	
gcc tct aca gtc agt gtg ggc tcc agt gag acc cgg ggt gag cgt gtt		1632	
Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val			
530	535	540	
att gat gct gtg cga ttc acc ctc cgc cag acc atc tct ttc cca ccc		1680	
Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro			
545	550	555	560

cga gat gag tgg aat gac ttc aac ttt gac atg gat gct cgc cgc aat Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn 565 570 575	1728
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tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn 20 25 30	96
ggc tcc tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser 35 40 45	144
gtc acg gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala 50 55 60	192
ctc tct cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro 65 70 75 80	240
cac agt ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala 85 90 95	288
acc tgg acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala 100 105 110	336
aag aca tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly 115 120 125	384
gct gtt atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr 130 135 140	432
gag gtg gtg aag cggtc ccc aac cat gag ctg agc cgt gaa ttc aac Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn 145 150 155 160	480

gag gga cag att gcc cct cct agt cat ttg att cga gta gag ggg aac		528	
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn			
165	170	175	
agc cat gcc cag tat gta gaa gat ccc atc aca gga aga cag agt gtg		576	
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val			
180	185	190	
ctg gta cct tat gag cca ccc cag gtt ggc act gaa ttc acg aca gtc		624	
Leu Val Pro Tyr Glu Pro Gln Val Gly Thr Glu Phe Thr Thr Val			
195	200	205	
ttg tac aat ttc atg tgt aac agc agt tgt gtt gga ggg atg aac cgc		672	
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg			
210	215	220	
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Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val			
225	230	240	
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Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg			
245	250	255	
gac agg aag gcg gat gaa gat agc atc aga aag cag caa gtt tcg gac		816	
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp			
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agt aca aag aac ggt gat ggt acg aag cgc ccg ttt cgt cag aac aca		864	
Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr			
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cat ggt atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat		912	
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp			
290	295	300	
gaa ctg tta tac tta cca gtg agg ggc cgt gag act tat gaa atg ctg		960	
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu			
305	310	315	320
ttg aag atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac		1008	
Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His			
325	330	335	
aca att gaa acg tac agg caa cag caa cag cag cag cac cac tta		1056	
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln His Gln His Leu			
340	345	350	
ctt cag aaa cag acc tca ata cag tct cca tct tca tat ggt aac agc		1104	
Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser			
355	360	365	
tcc cca cct ctg aac aaa atg aac agc atg aac aag ctg cct tct gtg		1152	
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val			
370	375	380	

agc cag ctt atc aac cct cag cag cgcc aac gcc ctc act cct aca acc 1200
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400

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 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415

cca atg gct gga gac atg aat gga ctc agc ccc acc cag gca ctc cct 1296
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430

ccc cca ctc tcc atg cca tcc acc tcc cac tgc aca ccc cca cct ccg 1344
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
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Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

ggc tcc tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc 144
Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

gtc acg gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct 192
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

ctc tct cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg 240
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

cac agt ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc 288
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

acc tgg acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca	336
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala	
100	105
aag aca tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga	384
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly	
115	120
125	
gct gtt atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg	432
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr	
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Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn	
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Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn	
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Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val	
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Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val	
195	200
205	
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Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg	
210	215
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Arg Pro Ile Leu Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val	
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Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg	
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Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp	
260	265
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Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr	
275	280
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cat ggt atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat	912
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp	
290	295
300	
gaa ctg tta tac tta cca gtg agg ggc cgt gag act tat gaa atg ctg	960
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu	
305	310
315	320

ttg aag atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His 325 330 335	1008
aca att gaa acg tac agg caa cag caa cag cag cag cac cag cac tta Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln His Gln His Leu 340 345 350	1056
ctt cag aaa cat ctc ctt tca gcc tgc ttc agg aat gag ctt gtg gag Leu Gln Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu 355 360 365	1104
ccc cgg aga gaa act cca aaa caa tct gac gtc ttc ttt aga cat tcc Pro Arg Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser 370 375 380	1152
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gaa agt tat tac aga tct gcc atg tcg cag agc acc cag aca agc gag Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu 35 40 45	144
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cct ata tgc tca gta cag ccc atc gag ttg aac ttt gtg gat gaa cct Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro 65 70 75 80	240
tcc gaa aat ggt gca aca aac aag att gag att agc atg gat tgt atc Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile 85 90 95	288

cgc atg caa gac tca gac ctc agt gac ccc atg tgg cca cag tac acg		336
Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr		
100	105	110
aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc		384
Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser		
115	120	125
tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc gtg acg		432
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr		
130	135	140
gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc ctc tct		480
Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser		
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160		
cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca cac agc		528
Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser		
165	170	175
ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc acc tgg		576
Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp		
180	185	190
acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg aag aca		624
Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr		
195	200	205
tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc gct gtt		672
Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val		
210	215	220
atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc gag gtt		720
Ile Arg Ala Met Pro Val Tyr Lys Ala Glu His Val Thr Glu Val		
225	230	235
240		
gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat gag gga		768
Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly		
245	250	255
cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac agc cat		816
Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His		
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gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg ctg gtc		864
Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val		
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cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc ctg tac		912
Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr		
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aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga cgt cca		960
Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro		
305	310	315
		320

att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly 325	330	335	1008
cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac cgg Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg 340	345	350	1056
aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac agc gca Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala 355	360	365	1104
aag aac ggc gat ggt acg aag cgc cct ttc cgt cag aat aca cac gga Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly 370	375	380	1152
atc cag atg act tcc atc aag aaa cgg aga tcc cca gat gat gag ctg Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu 385	390	395	1200
ctg tac cta cca gtg aga ggt cgt gag acg tac gag atg ttg ctg aag Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys 405	410	415	1248
atc aaa gag tca ctg gag ctc atg cag tac ctc cct cag cac acg atc Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile 420	425	430	1296
gaa acg tac agg cag cag cag cag cag cag cac cag cta ctt cag Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln 435	440	445	1344
aaa cag acc tcg atg cag tct cag tct tca tat ggc aac agt tcc cca Lys Gln Thr Ser Met Gln Ser Gln Ser Tyr Gly Asn Ser Ser Pro 450	455	460	1392
cct ctg aac aaa atg aac agc atg aac aag ctg cct tcc gtg agc cag Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln 465	470	475	1440
ctt atc aac cca cag cag cgc aat gcc ctc act ccc acc acc atg cct Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Met Pro 485	490	495	1488
gag ggc atg gga gcc aac att cct atg atg ggc act cac atg cca atg Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met 500	505	510	1536
gct gga gac atg aat gga ctc agc cct acc caa gct ctc cct cct cca Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro 515	520	525	1584
ctc tcc atg ccc tcc acc tcc cac tgc acc cca cca ccg ccc tac ccc Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro 530	535	540	1632

aca gac tgc agc att gtc agt ttc tta gca agg ttg ggc tgc tca tca		1680	
Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser			
545	550	555	560
tgc ctg gac tat ttc acg acc cag ggg ctg acc acc atc tat cag att		1728	
Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile			
565	570	575	
gag cat tac tcc atg gat gat ttg gca agt ctg aag atc cct gaa cag		1776	
Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln			
580	585	590	
ttc cga cat gcc atc tgg aag ggc atc ctg gac cac agg cag ctg cac		1824	
Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His			
595	600	605	
gac ttc tcc tca cct cct cat ctc ctg agg acc cca agt ggt gcc tct		1872	
Asp Phe Ser Ser Pro Pro His Leu Leu Arg Thr Pro Ser Gly Ala Ser			
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acc gtc agt gtg ggc tcc agt gag acc cgt ggt gaa cgt gtg atc gat		1920	
Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp			
625	630	635	640
gcc gtg cgc ttt acc ctc cgc cag acc atc tct ttt cca ccc cgt gac		1968	
Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp			
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gag tgg aat gat ttc aac ttt gac atg gat tct cgt cgc aac aag cag		2016	
Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ser Arg Arg Asn Lys Gln			
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cct tac atc cag cgt ttc ata gaa acc cca gct cat ttc tcg tgg aaa		96	
Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys			
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gaa agt tat tac aga tct gcc atg tcg cag agc acc cag aca agc gag		144	
Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu			
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cct ata tgc tca gta cag ccc atc gag ttg aac ttt gtg gat gaa cct Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro	65	70	75	240
tcc gaa aat ggt gca aca aac aag att gag att agc atg gat tgt atc Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile	85	90	95	288
cgc atg caa gac tca gac ctc agt gac ccc atg tgg cca cag tac acg Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr	100	105	110	336
aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser	115	120	125	384
tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc gtg acg Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr	130	135	140	432
gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc ctc tct Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser	145	150	155	480
160				
cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca cac agc Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser	165	170	175	528
ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc acc tgg Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp	180	185	190	576
acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg aag aca Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr	195	200	205	624
tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc gct gtt Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val	210	215	220	672
atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc gag gtt Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val	225	230	235	720
240				
gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat gag gga Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly	245	250	255	768
cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac agc cat Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His	260	265	270	816

gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg ctg gtc		864	
Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val			
275	280	285	
cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc ctg tac		912	
Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr			
290	295	300	
aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga cgt cca		960	
Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro			
305	310	315	320
att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc		1008	
Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly			
325	330	335	
cga cg ^g tgc ttt gag gcc cg ^g atc tgt gct tgc cca gga aga gac cg ^g		1056	
Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg			
340	345	350	
aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac agc gca		1104	
Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala			
355	360	365	
aag aac ggc gat ggt acg aag cg ^c cct ttc cgt cag aat aca cac gga		1152	
Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly			
370	375	380	
atc cag atg act tcc atc aag aaa cg ^g aga tcc cca gat gat gag ctg		1200	
Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu			
385	390	395	400
ctg tac cta cca gtg aga ggt cgt gag acg tac gag atg ttg ctg aag		1248	
Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys			
405	410	415	
atc aaa gag tca ctg gag ctc atg cag tac ctc cct cag cac acg atc		1296	
Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile			
420	425	430	
gaa acg tac agg cag cag cag cag cag cag cac cta ctt cag		1344	
Glu Thr Tyr Arg Gln Gln Gln Gln His Gln His Leu Leu Gln			
435	440	445	
aaa cag acc tcg atg cag tct cag tct tca tat ggc aac agt tcc cca		1392	
Lys Gln Thr Ser Met Gln Ser Gln Ser Tyr Gly Asn Ser Ser Pro			
450	455	460	
cct ctg aac aaa atg aac agc atg aac aag ctg cct tcc gtg agc cag		1440	
Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln			
465	470	475	480
ctt atc aac cca cag cag cgc aat gcc ctc act ccc acc acc atg cct		1488	
Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Met Pro			
485	490	495	

gag ggc atg gga gcc aac att cct atg atg ggc act cac atg cca atg 1536
 Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met
 500 505 510

gct gga gac atg aat gga ctc agc cct acc caa gct ctc cct cca 1584
 Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro
 515 520 525

ctc tcc atg ccc tcc acc tcc cac tgc acc cca cca ccg ccc tac ccc 1632
 Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Tyr Pro
 530 535 540

aca gac tgc agc att gtc agg att tgg caa gtc tga 1668
 Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 545 550 555

<210> 9
 <211> 1452
 <212> DNA
 <213> Murine sp.

<220>
 <221> CDS
 <222> (1)..(1449)

<400> 9
 atg aat ttt gaa act tca cgg tgt gcc acc cta cag tac tgc ccc gac 48
 Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 1 5 10 15

cct tac atc cag cgt ttc ata gaa acc cca gct cat ttc tcg tgg aaa 96
 Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30

gaa agt tat tac aga tct gcc atg tcg cag agc acc cag aca agc gag 144
 Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
 35 40 45

ttc ctc agc cca gag gtc ttc cag cat atc tgg gat ttt ctg gaa cag 192
 Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60

cct ata tgc tca gta cag ccc atc gag ttg aac ttt gtg gat gaa cct 240
 Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
 65 70 75 80

tcc gaa aat ggt gca aca aac aag att gag att agc atg gat tgt atc 288
 Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
 85 90 95

cgc atg caa gac tca gac ctc agt gac ccc atg tgg cca cag tac acg 336
 Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
 100 105 110

• •

aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc		384	
Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser			
115	120	125	
tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc gtg acg		432	
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr			
130	135	140	
gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc ctc tct		480	
Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser			
145	150	155	160
cca tcc cct gcc att ccc tcc aac aca gat tac ccc ggc cca cac agc		528	
Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser			
165	170	175	
ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc acc tgg		576	
Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp			
180	185	190	
acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg aag aca		624	
Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr			
195	200	205	
tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc gct gtt		672	
Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val			
210	215	220	
atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc gag gtt		720	
Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val			
225	230	235	240
gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat gag gga		768	
Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly			
245	250	255	
cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac agc cat		816	
Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His			
260	265	270	
gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg ctg gtc		864	
Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val			
275	280	285	
cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc ctg tac		912	
Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr			
290	295	300	
aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga cgt cca		960	
Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro			
305	310	315	320
att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc		1008	
Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly			
325	330	335	

<210> 10
<211> 1761
<212> DNA
<213> Murine sp.

<220>
<221> CDS
<222> (1)..(1758)

<400> 10
atg ttg tac ctg gaa aac aat gcc cag act caa ttt agt gag cca cag 48
Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
1 5 10 15

tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac 96
Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
20 25 30

ggc tcc tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc		144	
Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser			
35	40	45	
gtg acg gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc		192	
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala			
50	55	60	
ctc tct cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca		240	
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro			
65	70	75	80
cac agc ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc		288	
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala			
85	90	95	
acc tgg acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg		336	
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala			
100	105	110	
aag aca tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc		384	
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Gln Gly			
115	120	125	
gct gtt atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc		432	
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr			
130	135	140	
gag gtt gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat		480	
Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn			
145	150	155	160
gag gga cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac		528	
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn			
165	170	175	
agc cat gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtc		576	
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val			
180	185	190	
ctg gtc cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc		624	
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val			
195	200	205	
ctg tac aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga		672	
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg			
210	215	220	
cgt cca att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc		720	
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val			
225	230	235	240
ctg ggc cga cgg tgc ttt gag gcc cggt atc tgt gct tgc cca gga aga		768	
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg			
245	250	255	

gac	cgg	aag	gca	gat	gaa	gac	agc	atc	aga	aag	cag	caa	gta	tcg	gac		816
Asp	Arg	Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp		
			260			265			270								
agc	gca	aag	aac	ggc	gat	ggt	acg	aag	cgc	cct	ttc	cgt	cag	aat	aca		864
Ser	Ala	Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr		
			275			280			285								
cac	gga	atc	cag	atg	act	tcc	atc	aag	aaa	cg	aga	tcc	cca	gat	gat		912
His	Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp		
			290			295			300								
gag	ctg	ctg	tac	cta	cca	gtg	aga	ggt	cgt	gag	acg	tac	gag	atg	ttg		960
Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu		
			305			310			315			320					
ctg	aag	atc	aaa	gag	tca	ctg	gag	ctc	atg	cag	tac	ctc	cct	cag	cac		1008
Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His		
			325			330			335								
acg	atc	gaa	acg	tac	agg	cag	cag	cag	cag	cac	cac	cac	cta			1056	
Thr	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu			
			340			345			350								
ctt	cag	aaa	cag	acc	tcg	atg	cag	tct	cag	tct	tca	tat	ggc	aac	agt		1104
Leu	Gln	Lys	Gln	Thr	Ser	Met	Gln	Ser	Gln	Ser	Ser	Tyr	Gly	Asn	Ser		
			355			360			365								
tcc	cca	cct	ctg	aac	aaa	atg	aac	agc	atg	aac	aag	ctg	cct	tcc	gtg		1152
Ser	Pro	Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val		
			370			375			380								
agc	cag	ctt	atc	aac	cca	cag	cag	cgc	aat	gcc	ctc	act	ccc	acc	acc		1200
Ser	Gln	Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn	Ala	Leu	Thr	Pro	Thr	Thr		
			385			390			395			400					
atg	cct	gag	ggc	atg	gga	gcc	aac	att	cct	atg	atg	ggc	act	cac	atg		1248
Met	Pro	Glu	Gly	Met	Gly	Ala	Asn	Ile	Pro	Met	Met	Gly	Thr	His	Met		
			405			410			415								
cca	atg	gct	gga	gac	atg	aat	gga	ctc	agc	cct	acc	caa	gct	ctc	cct		1296
Pro	Met	Ala	Gly	Asp	Met	Asn	Gly	Leu	Ser	Pro	Thr	Gln	Ala	Leu	Pro		
			420			425			430			430					
cct	cca	ctc	tcc	atg	ccc	tcc	acc	tcc	cac	tgc	acc	cca	cca	ccg	ccc		1344
Pro	Pro	Leu	Ser	Met	Pro	Ser	Thr	Ser	His	Cys	Thr	Pro	Pro	Pro	Pro		
			435			440			445								
tac	ccc	aca	gac	tgc	agc	att	gtc	agt	ttc	tta	gca	agg	ttg	ggc	tgc		1392
Tyr	Pro	Thr	Asp	Cys	Ser	Ile	Val	Ser	Phe	Leu	Ala	Arg	Leu	Gly	Cys		
			450			455			460								
tca	tca	tgc	ctg	gac	tat	ttc	acg	acc	cag	ggg	ctg	acc	acc	atc	tat		1440
Ser	Ser	Cys	Leu	Asp	Tyr	Phe	Thr	Thr	Gln	Gly	Leu	Thr	Thr	Ile	Tyr		
			465			470			475			480					

cag att gag cat tac tcc atg gat ttg gca agt ctg aag atc cct		1488	
Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro			
485	490	495	
gaa cag ttc cga cat gcc atc tgg aag ggc atc ctg gac cac agg cag		1536	
Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln			
500	505	510	
ctg cac gac ttc tcc tca cct cat ctc ctg agg acc cca agt ggt		1584	
Leu His Asp Phe Ser Ser Pro Pro His Leu Leu Arg Thr Pro Ser Gly			
515	520	525	
gcc tct acc gtc agt gtg ggc tcc agt gag acc cgt ggt gaa cgt gtg		1632	
Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val			
530	535	540	
atc gat gcc gtg cgc ttt acc ctc cgc cag acc atc tct ttt cca ccc		1680	
Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro			
545	550	555	560
cgt gac gag tgg aat gat ttc aac ttt gac atg gat tct cgt cgc aac		1728	
Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ser Arg Arg Asn			
565	570	575	
aag cag cag cgt atc aaa gag gaa gga gaa tga		1761	
Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu			
580	585		

<210> 11
<211> 1386
<212> DNA
<213> Murine sp.

<220>
<221> CDS
<222> (1)..(1383)

<400> 11						
atg ttg tac ctg gaa aac aat gcc cag act caa ttt agt gag cca cag						48
Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln						
1	5	10	15			
tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac						96
Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn						
20	25	30				
ggc tcc tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc						144
Gly Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser						
35	40	45				
gtg acg gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc						192
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala						
50	55	60				

ctc tct cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca	240
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro	
65 70 75 80	
cac agc ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc	288
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala	
85 90 95	
acc tgg acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg	336
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala	
100 105 110	
aag aca tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc	384
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly	
115 120 125	
gct gtt atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc	432
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr	
130 135 140	
gag gtt gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat	480
Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn	
145 150 155 160	
gag gga cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac	528
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn	
165 170 175	
agc cat gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg	576
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val	
180 185 190	
ctg gtc cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc	624
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val	
195 200 205	
ctg tac aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga	672
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg	
210 215 220	
cgt cca att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc	720
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val	
225 230 235 240	
ctg ggc cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga	768
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg	
245 250 255	
gac cgg aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac	816
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp	
260 265 270	
agc gca aag aac ggc gat ggt acg aag cgc cct ttc cgt cag aat aca	864
Ser Ala Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr	
275 280 285	

cac gga atc cag atg act tcc atc aag aaa cg ^g aga tcc cca gat gat		912	
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp			
290	295	300	
gag ctg ctg tac cta cca gtg aga ggt cgt gag acg tac gag atg ttg		960	
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu			
305	310	315	320
ctg aag atc aaa gag tca ctg gag ctc atg cag tac ctc cct cag cac		1008	
Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His			
325	330	335	
acg atc gaa acg tac agg cag cag cag cag cac cac cag cta		1056	
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln His Gln His Leu			
340	345	350	
ctt cag aaa cag acc tcg atg cag tct cag tct tca tat ggc aac agt		1104	
Leu Gln Lys Gln Thr Ser Met Gln Ser Gln Ser Tyr Gly Asn Ser			
355	360	365	
tcc cca cct ctg aac aaa atg aac agc atg aac aag ctg cct tcc gtg		1152	
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val			
370	375	380	
agc cag ctt atc aac cca cag cag cgc aat gcc ctc act ccc acc acc		1200	
Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr			
385	390	395	400
atg cct gag ggc atg gga gcc aac att cct atg atg ggc act cac atg		1248	
Met Pro Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met			
405	410	415	
cca atg gct gga gac atg aat gga ctc agc cct acc caa gct ctc cct		1296	
Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro			
420	425	430	
cct cca ctc tcc atg ccc tcc acc tcc cac tgc acc cca cca ccg ccc		1344	
Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro			
435	440	445	
tac ccc aca gac tgc agc att gtc agg att tgg caa gtc tga		1386	
Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val			
450	455	460	

<210> 12
<211> 1170
<212> DNA
<213> Murine sp.

<220>
<221> CDS
<222> (1)...(1167)

<400> 12
 atg ttg tac ctg gaa aac aat gcc cag act caa ttt agt gag cca cag 48
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

 tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac 96
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

 ggc tcc tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc 144
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

 gtg acg gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc 192
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

 ctc tct cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca 240
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

 cac agc ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc 288
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

 acc tgg acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg 336
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

 aag aca tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc 384
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

 gct gtt atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc 432
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

 gag gtt gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat 480
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

 gag gga cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac 528
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175

 agc cat gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtc 576
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190

 ctg gtc cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc 624
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

 ctg tac aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga 672
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220

cgt cca att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc		720	
Arg Pro Ile Leu Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val			
225	230	235	240
ctg ggc cga cgg tgc ttt gag gcc cg ^g atc tgt gct tgc cca gga aga		768	
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg			
245	250	255	
gac cg ^g aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac		816	
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp			
260	265	270	
agc gca aag aac ggc gat gct ttc cgt cag aat aca cac gga atc cag		864	
Ser Ala Lys Asn Gly Asp Ala Phe Arg Gln Asn Thr His Gly Ile Gln			
275	280	285	
atg act tcc atc aag aaa cg ^g aga tcc cca gat gat gag ctg ctg tac		912	
Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr			
290	295	300	
cta cca gtg aga ggt cgt gag acg tac gag atg ttg ctg aag atc aaa		960	
Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys			
305	310	315	320
gag tca ctg gag ctc atg cag tac ctc cct cag cac acg atc gaa acg		1008	
Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr			
325	330	335	
tac agg cag cag cag cag cag cac cag cac cta ctt cag aaa cat		1056	
Tyr Arg Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His			
340	345	350	
ctc ctt tca gcc tgc ttc agg aat gag ctt gtg gag ccc cg ^g gga gaa		1104	
Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Gly Glu			
355	360	365	
gct ccg aca cag tct gac gtc ttc ttt aga cat tcc aac ccc cca aac		1152	
Ala Pro Thr Gln Ser Asp Val Phe Phe Arg His Ser Asn Pro Pro Asn			
370	375	380	
cac tcc gtg tac cca tag		1170	
His Ser Val Tyr Pro			
385			
<210> 13			
<211> 641			
<212> PRT			
<213> Homo sapiens			
<400> 13			
Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe			
1	5	10	15
Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro			
20	25	30	

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60

 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80

 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95

 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110

 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125

 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140

 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160

 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175

 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190

 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205

 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220

 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240

 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255

 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270

 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285

 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300

 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320

 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415

Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445

Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460

Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480

Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495

His Cys Thr Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
 500 505 510

Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525

Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540

Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560

Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575

Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590

Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605

Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
 610 615 620

Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640

Glu

<210> 14
<211> 516
<212> PRT
<213> Homo sapiens

<400> 14		
Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe		
1	5	10
		15
Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro		
20	25	30
Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn		
35	40	45
Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu		
50	55	60
Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser		
65	70	75
		80
Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn		
85	90	95
Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln		
100	105	110
Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser		
115	120	125
Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln		
130	135	140
Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys		
145	150	155
		160
Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val		
165	170	175
Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr		
180	185	190
Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His		
195	200	205
Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His		
210	215	220
Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro		
225	230	240
Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val		
245	250	255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Arg
 500 505 510
 Ile Trp Gln Val
 515

<210> 15
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15
 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30
 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45
 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320

Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350

Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365

Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
 405 410 415

Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
 420 425 430

Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
 435 440 445

<210> 16
 <211> 586
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220

Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240

Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255

Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270

Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285

His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300

Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320

Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335

Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350

Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365

Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380

Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400

Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415

Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430

Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445

Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys
 450 455 460

Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr
 465 470 475 480

Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
 485 490 495

Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
 500 505 510

Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser
 515 520 525

Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
 530 535 540

Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
 545 550 555 560

Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn
 565 570 575

Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
 580 585

<210> 17

<211> 461

<212> PRT

<213> Homo sapiens

<400> 17

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220

Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240

Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255

Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270

Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285

His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300

Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320

Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335

Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln His Gln His Leu
 340 345 350

Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365

Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380

Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400

Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415

Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430

Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445

Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 450 455 460

<210> 18
<211> 393
<212> PRT
<213> Homo sapiens

<400> 18

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Gln Gly
 115 120 125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220

Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240

Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255

Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270

Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285

His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300

Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320

Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335

Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln His Gln His Leu
 340 345 350

Leu Gln Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu
 355 360 365

Pro Arg Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser
 370 375 380

Lys Pro Pro Asn Arg Ser Val Tyr Pro
 385 390

<210> 19
 <211> 680
 <212> PRT
 <213> Murine sp.

<400> 19
 Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 1 5 10 15

Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30

Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
 35 40 45

Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60

Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
 65 70 75 80

Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu
 385 390 395 400

Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys
 405 410 415

Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile
 420 425 430

Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln
 435 440 445

Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser Ser Pro
 450 455 460

Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln
 465 470 475 480

Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Met Pro
 485 490 495

Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met
 500 505 510

Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro
 515 520 525

Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro
 530 535 540

Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser
 545 550 555 560

Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile
 565 570 575

Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln
 580 585 590

Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His
 595 600 605

Asp Phe Ser Ser Pro Pro His Leu Leu Arg Thr Pro Ser Gly Ala Ser
 610 615 620

Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp
 625 630 635 640

Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp
 645 650 655

Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ser Arg Arg Asn Lys Gln
 660 665 670

Gln Arg Ile Lys Glu Glu Gly Glu
 675 680

<210> 20
 <211> 555
 <212> PRT
 <213> Murine sp.

<400> 20
 Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 1 5 10 15

Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30

Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
 35 40 45

Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60

Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
 65 70 75 80

Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
 85 90 95

Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
 100 105 110

Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser
 115 120 125

Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr
 130 135 140

Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser
 145 150 155 160

Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser
 165 170 175

Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp
 180 185 190

Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr
 195 200 205

Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val
 210 215 220

Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val
 225 230 235 240

Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly
 245 250 255

Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His
 260 265 270
 Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val
 275 280 285
 Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr
 290 295 300
 Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro
 305 310 315 320
 Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly
 325 330 335
 Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg
 340 345 350
 Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala
 355 360 365
 Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly
 370 375 380
 Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu
 385 390 395 400
 Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys
 405 410 415
 Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile
 420 425 430
 Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln
 435 440 445
 Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser Ser Pro
 450 455 460
 Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln
 465 470 475 480
 Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Met Pro
 485 490 495
 Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met
 500 505 510
 Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro
 515 520 525
 Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro
 530 535 540
 Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 545 550 555

<210> 21
<211> 483
<212> PRT
<213> Murine sp.

<400> 21

Met	Asn	Phe	Glu	Thr	Ser	Arg	Cys	Ala	Thr	Leu	Gln	Tyr	Cys	Pro	Asp
1				5					10					15	

Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
20 25 30

Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
35 40 45

Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
50 55 60

Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
65 70 75 80

Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
85 90 95

Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
100 105 110

Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser
115 120 125

Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr
130 135 140

Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser
145 150 155 160

Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser
165 170 175

Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp
180 185 190

Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr
195 200 205

Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val
210 215 220

Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val
225 230 235 240

Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly
245 250 255

Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His
260 265 270

Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val
 275 280 285
 Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr
 290 295 300
 Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro
 305 310 315 320
 Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly
 325 330 335
 Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg
 340 345 350
 Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala
 355 360 365
 Lys Asn Gly Asp Ala Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr
 370 375 380
 Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro
 385 390 395 400
 Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser
 405 410 415
 Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg
 420 425 430
 Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu
 435 440 445
 Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Gly Glu Ala Pro
 450 455 460
 Thr Gln Ser Asp Val Phe Phe Arg His Ser Asn Pro Pro Asn His Ser
 465 470 475 480
 Val Tyr Pro

<210> 22
 <211> 586
 <212> PRT
 <213> Murine sp.

<400> 22
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175

 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190

 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220

 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240

 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255

 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270

 Ser Ala Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285

 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300

 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320

 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335

 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350

Leu Gln Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Met Pro Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys
 450 455 460
 Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr
 465 470 475 480
 Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
 485 490 495
 Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
 500 505 510
 Leu His Asp Phe Ser Ser Pro Pro His Leu Leu Arg Thr Pro Ser Gly
 515 520 525
 Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
 530 535 540
 Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
 545 550 555 560
 Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ser Arg Arg Asn
 565 570 575
 Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
 580 585
 <210> 23
 <211> 461
 <212> PRT
 <213> Murine sp.
 <400> 23
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350

Leu Gln Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser
 355 360 365

Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380

Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400

Met Pro Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415

Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430

Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445

Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 450 455 460

<210> 24
<211> 389
<212> PRT
<213> Murine sp.

<400> 24
Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220

Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240

Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255

Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270

Ser Ala Lys Asn Gly Asp Ala Phe Arg Gln Asn Thr His Gly Ile Gln
 275 280 285

Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr
 290 295 300

Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys
 305 310 315 320

Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr
 325 330 335

Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His
 340 345 350

Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Gly Glu
 355 360 365

Ala Pro Thr Gln Ser Asp Val Phe Phe Arg His Ser Asn Pro Pro Asn
 370 375 380

His Ser Val Tyr Pro
 385

<210> 25
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 25
 Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
 1 5 10 15

 Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
 20 25 30

 Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
 35 40 45

 Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
 50 55 60

 Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro
 65 70 80

 Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
 85 90 95

 Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
 100 105 110

 Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
 115 120 125

 Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
 130 135 140

 Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
 145 150 160

 Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
 165 170 175

 Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
 180 185 190

 His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
 195 200 205

 Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
 210 215 220

 Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
 225 230 240

 Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
 245 250 255

 Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
 260 265 270

 His Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
 275 280 285

 Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
 290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
 305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
 325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
 340 345 350

Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
 355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
 370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp
 385 390

<210> 26

<211> 499

<212> PRT

<213> Homo sapiens

<400> 26

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
 1 5 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
 20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
 50 55 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
 100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
 130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
 145 150 155 160

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg
 165 170 175

 Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
 180 185 190

 Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
 195 200 205

 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
 210 215 220

 Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
 225 230 235 240

 Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe
 245 250 255

 Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu
 260 265 270

 Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg
 275 280 285

 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
 290 295 300

 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala
 305 310 315 320

 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala
 325 330 335

 Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu
 340 345 350

 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu
 355 360 365

 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro
 370 375 380

 Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser
 385 390 395 400

 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys
 405 410 415

 Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
 420 425 430

 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val
 435 440 445

 Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly
 450 455 460

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
 465 470 475 480

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr
 485 490 495

Trp Gly Pro

<210> 27
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 primer

<220>
<221> modified_base
<222> (15)
<223> inosine

<400> 27
ggcctcgagt acaantwcat gtgtaayag 29

<210> 28
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 primer

<400> 28
ggcatcgatt ctcttccagg gcaaggcaca 29

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 primer

<400> 29
ggcatcgatg aactcacggc tcagctc 27

<210> 30
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 30
tttagtgagg gttataaagc ggccgcgtcg tgactggag cgc 43

<210> 31
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 31
gccctggagg cgccgcgtta ttaaccctca c 31

<210> 32
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 32
ggcatcgatg tagacaggca tggcacg 27

<210> 33
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 33
gggctcgagc tgaagaagct gtactgc 27

<210> 34
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 34	
gggatcgatc tccgtttctt gatggaa	27
<210> 35	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
primer	
<400> 35	
cctgcctgga cttgcctgg	19
<210> 36	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
primer	
<400> 36	
ccaggcaagt ccaggcagg	19
<210> 37	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
primer	
<400> 37	
gaacatgtcc caacatgttg	20
<210> 38	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
primer	
<400> 38	
caacatgttg ggacatgttc	20
<210> 39	

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 39
ccttaatggc ctttaatgg 19

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 40
ccattaaagt ccattaagg 19

<210> 41
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 41
atgtcccaga gccacacag 19

<210> 42
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 42
agctcatggt tggggcac 18

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 43
cagactcaat ttagtgag 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 44
agctcatggg tggggcac 18

<210> 45
<211> 120
<212> PRT
<213> Murine sp.

<400> 45
Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
1 5 10 15

Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
20 25 30

Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
35 40 45

Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
50 55 60

Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
65 70 75 80

Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
85 90 95

Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
100 105 110

Asn Leu Gly Leu Leu Asn Ser Met
115 120

<210> 46
<211> 81
<212> PRT
<213> Homo sapiens

<400> 46

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80

Met

<210> 47

<211> 26

<212> PRT

<213> Homo sapiens

<400> 47

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met
 20 25

<210> 48

<211> 245

<212> PRT

<213> Homo sapiens

<400> 48

Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr
 1 5 10 15

Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn
 20 25 30

Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn
 35 40 45

Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met
 50 55 60

Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp
 65 70 75 80

Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met
 85 90 95

Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys
 100 105 110

Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp
 115 120 125
 Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr
 130 135 140
 Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His
 145 150 155 160
 Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser
 165 170 175
 Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser
 180 185 190
 Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg
 195 200 205
 Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn
 210 215 220
 Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile
 225 230 235 240
 Lys Glu Glu Gly Glu
 245

<210> 49
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 49
 Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr
 1 5 10 15
 Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn
 20 25 30
 Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn
 35 40 45
 Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met
 50 55 60
 Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp
 65 70 75 80
 Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met
 85 90 95
 Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys
 100 105 110

Ser Ile Val Arg Ile Trp Gln Val
115 120

<210> 50
<211> 52
<212> PRT
<213> Homo sapiens

<400> 50
Arg Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu
1 5 10 15

Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr
20 25 30

Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg
35 40 45

Ser Val Tyr Pro
50

<210> 51
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 51
atgcccagag cacacag 17

<210> 52
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 52
tccaccaccc tggctgtta g 21

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 53
gaccacagtc catgacatca ct

22